



SEQUENCE LISTING

<110> CVITKOVITCH, Dennis

<120> SIGNAL PEPTIDES NUCLEIC ACID MOLECULES AND METHODS FOR TREATMENT OF CARIE
S

<130> 1889/00401

<140> 09/833,017

<141> 2001-04-10

<160> 30

<170> PatentIn version 3.0

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<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(141)

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gat gaa tta gag att atc att ggc gga agc gga agc cta tca aca ttt 96
Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

ttc cgg ctg ttt aac aga agt ttt aca caa gct ttg gga aaa taa 141
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35 40 45

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<212> PRT

<213> Streptococcus mutans

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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

<210> 3

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 <213> Streptococcus mutans

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Gln Ala Leu Gly Lys
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acc gtt cta ttt ctc ttg ttt cta ttt tct aag gta agt aat gtc act 96
 Thr Val Leu Phe Leu Leu Phe Leu Phe Ser Lys Val Ser Asn Val Thr
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tta tcg aaa aag gaa tta act ctt ttt tcg ata agc aat ttt ctg ata 144
 Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
 35 40 45

atg att gct gtt acg atg gtg aac gta aac ctg ttt tat cct gca gag 192
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 50 55 60

cct ctt tat ttt ata gct tta tca att tat ctt aat aga cag aat agt 240
 Pro. Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
 65 70 75 80
 ctt tct cta aat ata ttt tat ggt ctg ctg cct gtt gcc agt tct gac 288
 Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp
 85 90 95
 ttg ttt agg cgg gca atc ata ttc ttt atc ttg gat gga act caa gga 336
 Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly
 100 105 110
 att gta atg ggc agt agc att ata acc acc tat atg atc gag ttt gca 384
 Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala
 115 120 125
 gga ata gcg cta agt tac ctc ttt ctc agt gtg ttc aat gtt gat att 432
 Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile
 130 135 140
 ggt cga ctt aaa gat agt ttg acc aag atg aag gtc aaa aaa cgc ttg 480
 Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu
 145 150 155 160
 att cca atg aat att act atg ctt cta tac tac ctt tta ata cag gta 528
 Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val
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 ttg tat gtt ata gag agt tat aat gtg ata ccg act tta aaa ttt cgt 576
 Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg
 180 185 190
 aaa ttt gtc gtt att gtc tat ctt att tta ttt ttg att ctg atc tca 624
 Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser
 195 200 205
 ttt tta agc caa tat acc aaa caa aag gtt caa aat gag ata atg gca 672
 Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala
 210 215 220
 caa aag gaa gct cag att cga aat atc acc cag tat agt cag caa ata 720
 Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile
 225 230 235 240
 gaa tct ctt tac aag gat att cga agt ttc cgc cat gat tat ctg aat 768
 Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn
 245 250 255
 att tta act agc ctc aga tta ggc att gaa aat aaa gat tta gct agt 816
 Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser
 260 265 270
 att gaa aag att tac cat caa atc tta gaa aaa aca gga cat caa ttg 864
 Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu
 275 280 285
 cag gat acc cgt tat aat atc ggc cat cta gct aat att caa aac gat 912
 Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp
 290 295 300

gct gtc aag ggt atc ttg tca gca aaa atc tta gaa gct cag aat aaa 960
Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys
305 310 315 320

aag att gct gtc aat gta gaa gtc tca agt aaa ata caa ctg cct gag 1008
Lys Ile Ala Val Asn Val Glu Val Ser Lys Ile Gln Leu Pro Glu
325 330 335

atg gag ttg ctt gat ttc att acc ata ctt tct atc ttg tgt gat aat 1056
Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn
340 345 350

gcc att gag gct gct ttc gaa tca tta aat cct gaa att cag tta gcc 1104
Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
355 360 365

ttt ttt aag aaa aat ggc agt ata gtc ttt atc att cag aat tcc acc 1152
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370 375 380

aaa gaa aaa caa ata gat gtg agt aaa att ttt aaa gaa aac tat tcc 1200
Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser
385 390 395 400

act aaa ggc tcc aat cgc ggt att ggt tta gca aag gtg aat cat att 1248
Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
405 410 415

ctt gaa cat tat ccc aaa acc agt tta caa aca agc aat cat cat cat 1296
Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His
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435 440

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<212> PRT
<213> Streptococcus mutans

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Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
35 40 45

Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
50 55 60

Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
65 70 75 80

Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp
85 90 95

Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly
100 105 110

Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala
115 120 125

Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile
130 135 140

Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu
145 150 155 160

Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val
165 170 175

Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg
180 185 190

Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser
195 200 205

Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala
210 215 220

Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile
225 230 235 240

Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn
245 250 255

Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser
260 265 270

Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu
275 280 285

Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp

290

295

300

Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys
305 310 315 320

Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu
325 330 335

Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn
340 345 350

Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
355 360 365

Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr
370 375 380

Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser
385 390 395 400

Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
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Leu Phe Lys Gln Leu Leu Ile Ile Lys
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ctt gaa acc acc att gca gct atc atg aaa gaa aaa aat tgg tct tat 96
Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr
20 25 30

aaa gaa ttg act att ttt gga aaa cca caa caa ctt att gac gct atc 144
Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile

35

40

45

cct gaa aag ggc aat cac cag att ttc ttt ttg gat att gaa atc aaa 192
 Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys
 50 55 60

aaa gag gaa aag aaa gga ctg gaa gta gcc aat cag att aga cag cat 240
 Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His
 65 70 75 80

aat cct agt gca gtt att gtc ttt gtc acg aca cat tct gag ttt atg 288
 Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met
 85 90 95

ccc ctc act ttt cag tat cag gta tct gct ttg gat ttt att gat aaa 336
 Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys
 100 105 110

tct ttg aat cct gag gag ttc tcc cac cgc att gaa tca gcg ctg tat 384
 Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr
 115 120 125

tat gct atg gaa aac agc cag aag aat ggt caa tca gag gaa ctt ttt 432
 Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe
 130 135 140

att ttc cat tca tct gaa act cag ttt cag gtc cct ttt gct gag att 480
 Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile
 145 150 155 160

ctg tat ttt gaa aca tct tca aca gcc cat aag ctc tgc ctt tat act 528
 Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr
 165 170 175

tat gat gaa cgg att gaa ttc tac ggc agt atg act gac att gtt aaa 576
 Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys
 180 185 190

atg gat aag aga ctt ttt cag tgc cat cgc tct ttt att gtc aat cct 624
 Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro
 195 200 205

gcc aat att acc cgt att gat cgg aaa aaa cgc ttg gcc tat ttt cga 672
 Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg
 210 215 220

aat aat aag tct tgt ctt att tca cga act aag tta aca aaa ctg aga 720
 Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg
 225 230 235 240

gct gtg att gct gat caa agg aga gca aaa 750
 Ala Val Ile Ala Asp Gln Arg Arg Ala Lys
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<210> 8

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<212> PRT

<213> Streptococcus mutans

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Met Ile Ser Ile Phe Val Leu Glu Asp Asp Phe Leu Gln Gln Gly Arg
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Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr
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Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile
 35 40 45

Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys
 50 55 60

Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His
 65 70 75 80

Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met
 85 90 95

Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys
 100 105 110

Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr
 115 120 125

Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe
 130 135 140

Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile
 145 150 155 160

Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr
 165 170 175

Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys
 180 185 190

Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro
 195 200 205

Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg
 210 215 220

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225 230 235 240

Ala Val Ile Ala Asp Gln Arg Arg Ala Lys
245 250

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<213> Streptococcus mutans

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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<213> Streptococcus mutans

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<222> (1) .. (46)

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20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
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Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Thr Leu Ser Thr Phe
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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala
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<222> (1)..(46)

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Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
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Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
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Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
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Gln Ala Leu Gly Lys
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<212> DNA

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24

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<400> 20
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 <212> DNA
 <213> Streptococcus mutans

<220>
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 <222> (1)..(408)

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tgg aaa tta agc cgt tat tac ttt att aaa atg tgg act cgt gaa gat 96
 Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp
 20 25 30

tgg caa caa gag gga atg ttg att ttg cac caa tta tta agg gaa cat 144
 Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His
 35 40 45

cca gaa tta gaa gag gat gat aca aaa ttg tat atc tat ttt aag aca 192
 Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr
 50 55 60

cgt ttt tct aat tac att aaa gat gtt ttg cgt cag caa gaa agt cag 240
 Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln
 65 70 75 80

aaa cgt cgt ttt aat aga atg tct tat gaa gaa gtc ggt gag att gaa 288
 Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu
 85 90 95

cac tgt ttg tca agt ggc ggt atg caa ttg gat gaa tat att tta ttt 336
 His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe
 100 105 110

cgt gat agt ttg ctt gca tat aaa caa ggt ctg agt act gaa aag caa 384
 Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln
 115 120 125

gag ctg ttt gag cgc ttg gta gca ggagagcact ttttggaag gcaaagtatg 438
 Glu Leu Phe Glu Arg Leu Val Ala
 130 135

ctgaaagatt tacgtaaaaa attaagtgat ttttaaggaaa aa 480

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 <211> 136
 <212> PRT
 <213> Streptococcus mutans
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Met Glu Glu Asp Phe Glu Ile Val Phe Asn Lys Val Lys Pro Ile Val
 1 5 10 15

Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp
 20 25 30

Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His
 35 40 45

Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr
 50 55 60

Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln

[illegible]

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<212>	DNA
<213>	Streptococcus mutans

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tgtttttaat aaggттаагс сaatтgtatg гaaаттаагс сgttat tact ttattaaat	180
gtggactcgt gaagattggc асаагаggg aatgttgatt ttgcaccaat тattaaggga	240
acatccagaa ttagaagagg атgатасаа атtgtatatc таттttaага саgttttttc	300
taattacatt aaagatgttt tgсgtcagca агaaagtcag ааасgtсgtt ттаатагаат	360
gtcttatgaa gaagtcggtg агattгааса ctgtttgtca агtgggcggta tgcaattgga	420
tgaatatatt ttatttctgt атagtttgct tgcatataaa caagggtcta gtactgaaaa	480
gcaagagctg tttagcgcct tggtagcagg агagcacttt ttgggaaggc aaagtatgct	540
gaaagattta cgtaaaaaat таagtгаттт таaggааааа таgttaaaaa gggaagaat	600
ggaacatgtg attgtaccat tctttttggt tgaaaattaa gaaaagttat tataaattat	660
tggtttaaca tgccatatta	680

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<211> 2280
<212> DNA
<213> Streptococcus mutans
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<220>

<221> CDS

<222> (1)...(2280)

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Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile
1 5 10 15

ctc tta gag att atc aaa aga gta aca aaa agg gga ggg aca gtt tcg 96
Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
20 25 30

tca tct aat cct tta cca gat ggg cag tct aag ttg ttt tgg cgc aga 144
Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg
35 40 45

cat tat aag cta gta cct cag att gat acc aga gac tgt ggg ccg gca 192
His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala
50 55 60

gtg ctg gca tct gtt gca aag cat tac gga tct aat tac tct atc gct 240
Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala
65 70 75 80

tat ctg cgg gaa ctc tca aag act aac aag cag gga aca aca gct ctt 288
Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu
85 90 95

ggc aat gtt gaa gct gct aaa aag tta ggc ttt gaa aca cgc tct atc 336
Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile
100 105 110

aag gcg gat atg acg ctt ttt gat tat aat gat ttg acc tat cct ttt 384
Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe
115 120 125

atc gtc cat gtg att aaa gga aaa cgt ctg cag cat tat tat gtc gtc 432
Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val
130 135 140

tat ggc agc cag aat aat cag ctg att att gga gat cct gat cct tca 480
Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser
145 150 155 160

gtt aag gtg act agg atg agt aag gaa cgc ttt caa tca gag tgg aca 528
Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr
165 170 175

ggc ctt gca att ttc cta gct cct cag cct aac tat aag cct cat aaa 576
Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys
180 185 190

ggc gaa aaa aat ggt ttg tct aat ttc ttc ccg ttg atc ttt aag cag 624
Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln
195 200 205

aaa gct ttg atg act tat att atc ata gct agc ttg att gtg acg ctc 672
Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu

210 215 220
 att gat att gtc gga tca tac tat ctc caa gga ata ttg gac gag tac 720
 Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr
 225 230 235 240
 att cct gat cag ctg att tca act tta gga atg att acg att ggt ctg 768
 Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu
 245 250 255

 ata ata acc tat att atc cag cag gtc atg gct ttt gca aaa gaa tac 816
 Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr
 260 265 270
 ctc ttg gcc gta ctc agt ttg cgt tta gtc att gat gtt atc ctg tct 864
 Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser
 275 280 285
 tat atc aaa cat att ttt acg ctt cct atg tct ttc ttt gcg aca agg 912
 Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg
 290 295 300
 cga aca gga gaa atc acg tct cgt ttt aca gat gcc aat cag att att 960
 Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile
 305 310 315 320
 gat gct gta gcg tca acc atc ttt tca atc ttt tta gat atg act atg 1008
 Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met
 325 330 335
 gta att ttg gtt ggt ggg gtt ttg ttg ggg caa aac aat aac ctt ttc 1056
 Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe
 340 345 350
 ttt cta acc ttg ctc tcc att ccg att tat gcc atc att att ttt gct 1104
 Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala
 355 360 365
 ttc ttg aaa ccc ttt gag aaa atg aat cac gaa gtg atg gaa agc aat 1152
 Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn
 370 375 380
 gct gtg gta agt tct tct atc att gaa gat atc aat ggg atg gaa acc 1200
 Ala Val Val Ser Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr
 385 390 395 400
 att aaa tca ctc aca agt gag tcc gct cgt tat caa aac att gat agt 1248
 Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser
 405 410 415
 gaa ttt gtt gat tat ttg gag aaa aac ttt aag cta cac aag tat agt 1296
 Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser
 420 425 430
 gcc att caa acc gca tta aaa agc ggt gct aag ctt atc ctc aat gtt 1344
 Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val
 435 440 445
 gtc att ctc tgg tat ggc tct cgt cta gtt atg gat aat aaa atc tca 1392

Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser
 450 455 460
 gtt ggt cag ctt atc acc ttt aat gct ttg ctg tct tat ttc tca aat 1440
 Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn
 465 470 475 480
 cca att gaa aat att atc aat ctg caa tcc aaa ctg cag tca gct cgc 1488
 Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg
 485 490 495
 gtt gcc aat aca cgt ctt aat gag gtc tat ctt gtc gaa tct gaa ttt 1536
 Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe
 500 505 510
 gaa aaa gac ggc gat tta tca gaa aat agc ttt tta gat ggt gat att 1584
 Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile
 515 520 525
 tcg ttt gaa aat ctt tct tat aaa tat gga ttt ggg cga gat acc tta 1632
 Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu
 530 535 540
 tca gat att aat tta tca atc aaa aaa ggc tcc aag gtc agt cta gtt 1680
 Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val
 545 550 555 560
 gga gcc agt ggt tct ggt aaa aca act ttg gct aaa ctg att gtc aat 1728
 Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn
 565 570 575
 ttc tac gag cct aac aag ggg att gtt cga atc aat ggc aat gat tta 1776
 Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu
 580 585 590
 aaa gtt att gat aag aca gct ttg cgg cgg cat att agc tat ttg ccg 1824
 Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro
 595 600 605
 caa cag gcc tat gtt ttt agt ggc tct att atg gat aat ctc gtt tta 1872
 Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu
 610 615 620
 gga gct aaa gaa gga acg agt cag gaa gac att att cgt gct tgt gaa 1920
 Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu
 625 630 635 640
 att gct gaa atc cgc tcg gac att gaa caa atg cct cag ggc tat cag 1968
 Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln
 645 650 655
 aca gag tta tca gat ggt gcc ggt att tct ggc ggt caa aaa cag cgg 2016
 Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg
 660 665 670
 att gct tta gct agg gcc tta tta aca cag gca ccg gtt ttg att ctg 2064
 Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu
 675 680 685

gat gaa gcc acc agc agt ctt gat att ttg aca gaa aag aaa att atc 2112
 Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile
 690 695 700

agc aat ctc tta cag atg acg gag aaa aca ata att ttt gtt gcc cac 2160
 Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His
 705 710 715 720

cgc tta agc att tca cag cgt act gac gaa gtc att gtc atg gat cag 2208
 Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln
 725 730 735

gga aaa att gtt gaa caa ggc act cat aag gaa ctt tta gct aag caa 2256
 Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln
 740 745 750

ggt ttc tat tat aac ctg ttt aat 2280
 Gly Phe Tyr Tyr Asn Leu Phe Asn
 755 760

<210> 28

<211> 760

<212> PRT

<213> Streptococcus mutans

<400> 28

Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile
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Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
 20 25 30

Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg
 35 40 45

His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala
 50 55 60

Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala
 65 70 75 80

Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu
 85 90 95

Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile
 100 105 110

Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe
 115 120 125

Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val
130 135 140

Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser
145 150 155 160

Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr
165 170 175

Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys
180 185 190

Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln
195 200 205

Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu
210 215 220

Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr
225 230 235 240

Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu
245 250 255

Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr
260 265 270

Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser
275 280 285

Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg
290 295 300

Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile
305 310 315 320

Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met
325 330 335

Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe
340 345 350

Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala
355 360 365

Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn
370 375 380

Ala Val Val Ser Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr
385 390 395 400

Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser
405 410 415

Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser
420 425 430

Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val
435 440 445

Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser
450 455 460

Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn
465 470 475 480

Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg
485 490 495

Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe
500 505 510

Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile
515 520 525

Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu
530 535 540

Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val
545 550 555 560

Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn
565 570 575

Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu
580 585 590

Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro

595

600

605

Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu
610 615 620

Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu
625 630 635 640

Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln
645 650 655

Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg
660 665 670

Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu
675 680 685

Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile
690 695 700

Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His
705 710 715 720

Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln
725 730 735

Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln
740 745 750

Gly Phe Tyr Tyr Asn Leu Phe Asn
755 760

<210> 29
<211> 900
<212> DNA
<213> Streptococcus mutans

<220>
<221> CDS
<222> (1)..(900)

<400> 29

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Met Asp Pro Lys Phe Leu Gln Ser Ala Glu Phe Tyr Arg Arg Arg Tyr
1 5 10 15

48

cat aat ttt gcg aca cta tta att gtt cct ttg gtc tgc ttg att atc
His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile

96

20	25	30	
ttc ttg gtc ata ttc ctt tgt ttt gct aaa aaa gaa att aca gtg att Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile 35 40 45			144
tct act ggt gaa gtt gca cca aca aag gtt gta gat gtt atc caa tct Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser 50 55 60			192
tac agt gac agt tca atc att aaa aat aat tta gat aat aat gca gct Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala 65 70 75 80			240
gtt gag aag gga gac gtt tta att gaa tat tca gaa aat gcc agt cca Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro 85 90 95			288
aac cgt cag act gaa caa aag aat att ata aaa gaa aga caa aaa cga Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg 100 105 110			336
gaa gag aag gaa aag aaa aaa cac caa aag agc aag aaa aag aag aag Glu Glu Lys Glu Lys Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys 115 120 125			384
tct aag agc aag aaa gct tcc aaa gat aag aaa aag aaa tcg aaa gac Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Lys Ser Lys Asp 130 135 140			432
aag gaa agc agc tct gac gat gaa aat gag aca aaa aag gtt tcg att Lys Glu Ser Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile 145 150 155 160			480
ttt gct tca gaa gat ggt att att cat acc aat ccc aaa tat gat ggt Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly 165 170 175			528
gcc aat att att ccg aag caa acc gag att gct caa atc tat cct gat Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp 180 185 190			576
att caa aaa aca aga aaa gtg tta atc acc tat tat gct tct tct gat Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp 195 200 205			624
gat gtt gtt tct atg aaa aag ggg caa acc gct cgt ctt tcc ttg gaa Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu 210 215 220			672
aaa aag gga aat gac aag gtt gtt att gaa gga aaa att aac aat gtc Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val 225 230 235 240			720
gct tca tca gca act act act aaa aaa gga aat ctc ttt aag gtt act Ala Ser Ser Ala Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr 245 250 255			768
gcc aaa gta aag gtt tct aag aaa aat agc aaa ctc atc aag tat ggt			816

Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly
260 265 270

atg aca ggc aag aca gtc act gtc att gat aaa aag act tat ttt gat 864
Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp
275 280 285

tat ttc aaa gat aaa tta ctg cat aaa atg gat aat 900
Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn
290 295 300

<210> 30
<211> 300
<212> PRT
<213> Streptococcus mutans

<400> 30

Met Asp Pro Lys Phe Leu Gln Ser Ala Glu Phe Tyr Arg Arg Arg Tyr
1 5 10 15

His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile
20 25 30

Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile
35 40 45

Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser
50 55 60

Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala
65 70 75 80

Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro
85 90 95

Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg
100 105 110

Glu Glu Lys Glu Lys Lys Lys His Gln Lys Ser Lys Lys Lys Lys
115 120 125

Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Lys Ser Lys Asp
130 135 140

Lys Glu Ser Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile
145 150 155 160

Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly
165 170 175

Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp
180 185 190

Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp
195 200 205

Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu
210 215 220

Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val
225 230 235 240

Ala Ser Ser Ala Thr Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr
245 250 255

Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly
260 265 270

Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp
275 280 285

Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn
290 295 300

Sub
Gly